SEQUENCE LISTING

<110> Selecore GmbH <120> Method for the identification of enzymes with desired characteristics by anchoring the reaction products on the surface of enzyme-presenting organisms <130> H2768 PCT S3 <150> EP 03023953.7 <151> 2003-10-22 <160> 2												
products on the surface of enzyme-presenting organisms <130> H2768 PCT S3 <150> EP 03023953.7 <151> 2003-10-22												
<130> H2768 PCT S3 <150> EP 03023953.7 <151> 2003-10-22												
<150> EP 03023953.7 <151> 2003-10-22												
<151> 2003-10-22												
•												
<160> 2												
170> PatentIn version 3.1												
<210> 1												
1> 2173 2> DNA												
<213> Pseudomonas aeruginosa												
<220>												
<221> CDS <222> (206)(2143)												
<223>												
<400> 1.												
gaagaagatc ggcctgtggg cggtacttct gctgggggtc gctctgctgg taataatggc 60												
aatgagcctg ctgcgttcct cgccgaacaa gccatgagcc ggttccgcgc tatgctgttc 120												
ggctgaggag gctttacgac gggccccggg gcgcatgccg acgacgcggc ggcccgacaa 180												
taaaaacaaa tcatggagta agaga atg atc aga atg gcg ctc aag cca ctg · 232												
Met Ile Arg Met Ala Leu Lys Pro Leu 1 5												
gta geg ged tgd etg get teg etg ted acc ged eeg eag get get 280												
Val Ala Ala Cys Leu Leu Ala Ser Leu Ser Thr Ala Pro Gln Ala Ala												
10 15 20 25												
cct tcg ccc tat tcg acg ctg gtg gtg ttc ggc gac agc ctc agc gat 328 Pro Ser Pro Tyr Ser Thr Leu Val Val Phe Gly Asp Ser Leu Ser Asp												
30 35 40												
goo ggg cag tto coc gat cot goo gge coc goo gga ago aco tog cgt 376												
Ala Gly Gln Phe Pro Asp Pro Ala Gly Pro Ala Gly Ser Thr Ser Arg 45 50 55												
ttc acc aac cgg gtc ggc ccg acc tac cag aac ggc agc ggc gag atc 424 Phe Thr Asn Arg Val Gly Pro Thr Tyr Gln Asn Gly Ser Gly Glu Ile												
60 65 70												
tte gga eeg ace geg eee atg etg ete gge aat eag ete gge ate gee 472												
Phe Gly Pro Thr Ala Pro Met Leu Gly Asn Gln Leu Gly Ile Ala 75 80 85												
cog ggt gac etg get gee teg ace teg eeg gte aac gee cag egg 520												

Pr	Gly	Asp	Leu	Ala	Ala 95	Ser	Thr	Ser	Pro	Val 100	Asn	Ala	Gln	Gln	Gly 105	•
	e gcc e Ala															568
	tac Tyr	-	_				_			_	_		-	-	-	616
	acc Thr															664
	ggc Gly 155	_		_	_	_			_							712
	aac Asn													Āla		760
	gcc Ala				Leu											808
-	gcg Ala								-			_		_		856
	gct Ala															904
	acg Thr 235															952
	gtc Val															1000
aac Asr	ccg Pro	gct Ala	tcc Ser	ttc Phe 270	ggc	ctg Leu	gcc Ala	gcc Ala	gac Asp 275	cag Gln	aac Asn	ctg Leu	atc Ile	ggc Gly 280	acc Thr	1048
tgt Cys	ttc Phe	agc Ser	ggc Gly 285	aac Asn	gąc Gly	tạc Cys	acc Thr	atg Met 290	aac Asn	ccg Pro	acc Thr	tac Tyr	ggg Gly 295	atc Ile	aac Asn	1096
Gly	agc Ser	acg Thr 300	ccc Pro	gac Asp	ccg Pro	agc Ser	aaa Lys 305	ttg Leu	ctg Leu	ttc Phe	aac Asn	gac Asp 310	agc Ser	gtg Val	cac His	1144
	acc Thr 315															1192
ctg	tcg	gcg	ccc	tgg	gag	ctg	acc	ctg	ctg	ccg	gaa	atg	gcc	cac	ggc	1240

Leu 330	Ser	Ala	Pro	Trp	Glu 335	Leu	Thr	Leu	Leu	Pro 340	Glu	Met	Ala	His	Gly 345	
					cag Gln											1288
				_	aac Asn	_				_			_			1336
		_	_	_	gac Asp		_		_	_	-	_	-	_		1384
-					aac Asn	-					-		_		-	1432
				-	ggg Gly 415	_							_	_	_	1480
					gat Asp											1528
agc Ser	gcc Ala	ttc Phe	gtg Val 445	cag Gln	tac Tyr	cag Gln	gaa Glu	aac Asn 450	cgc Arg	tgg Trp	tgg Trp	gcc Ala	gac Asp 455	gcg Ala	gcg Ala	1576
					ctc Leu											1624
ctg Leu	ggc Gly 475	ggc Gly	ggc Gly	gag Glu	cgc Arg	agc Ser 480	gag Glu	aaa Lys	ggc Gly	gac Asp	acc Thr 485	aac Asn	ggc Gly	cac His	ctg Leu	1672
tgg Trp 490	gcg Ala	ttc Phe	agc Ser	gcg Ala	cgc Arg 495	ctg Leu	ggc Gly	tac Tyr	gac Asp	atc Ile 500	gcc Ala	cag Gln	cag Gln	gcc Ala	gac Asp 505	1720
agt Ser	CCC Pro	tgg Trp	cac His	ctg Leu 510	tcg Ser	ccg Pro	ttc Phe	gtc Val	agc Ser 515	Ala	gac Asp	tat Tyr	gca Ala	cgg Arg 520	gtc Val	1768
gag Glu	gtc Val	gac Asp	ggc Gly 525	tat Tyr	tcc Ser	gag Glu	aag Lys	ggc Gly 530	gcc Ala	agc Ser	gcc Ala	acc Thr	gcg Ala 535	ctc Leu	gac Asp	1816
tac Tyr	gac Asp	gac Asp 540	cag Gln	aag Lys	cgc Arg	agc Ser	tcg Ser 545	aag Lys	cgc Arg	ctg Leu	ggc Gly	gcc Ala 550	ggc Gly	ctg Leu	caa Gln	1864
Gly	Lys 555	Tyr	Ala	Phe	ggc Gly	Ser 560	Asp	Thr	Gln	Leu	Phe 565	Ala	Glu	Tyr	Ala	1912
cac	gaa	cgt	gag	tac	gag	gac	gac	acc	cag	gac	ctg	acc	atg	tcc	ctc	1960

His 570		Arg	G1u	Tyr	Glu 575	Asp	Asp	Thr	Gln	Asp 580	Leu	Thr	Met	Ser	Leu 585		
		ctg Leu														2	2008
gac Asp	cat His	ctc Leu	aac Asn 605	cgc Arg	gtc Val	tca Ser	ctc Leu	ggc Gly 610	ttc Phe	agc Ser	cag Gln	aag Lys	ctg Leu 615	gcg Ala	ccg Pro	2	2056
		tcg Ser 620														2	2104
		cag Gln				-		-	_	_	-		tgaa	aacg	jcg	2	153
gccggcgccc ggtcggcgcc														2	173		
<21 <21 <21 <21	1> (2>)	2 646 PRT Pseud	lomor	nas a	erug	jinos	s a										
<40	0> :	2															
Met 1	Ile	Arg	Met	Ala 5	Leu	Lys	Pro	Leu	Val 10	Ala	Ala	Суз	Leu	Leu 15	Ala		
Ser	Leu	Ser	Thr 20	Ala	Pro	Gln	Ala	Ala 25	Pro	Ser	Pro		Ser 30	Thr	Leu		
Val	Val	Phe 35	Gly	Asp	Ser	Leu	Ser 40	Asp	Ala	Gly	Gln	Phe 45	Pro	Asp	Pro		
Ala	Gly 50	Pro	Ala	Gly	Ser	Thr 55	Ser	Arg	·Phe	Thr	Asn 60	Arg	Val	Gly	Pro		
Thr 65	Tyr	Gln	Asn	Gly	Ser 70	Gly	Glu	Ile	Phe	Gly 75	Pro	Thr	Ala	Pro	Met 80		
Leu	Leu	Gly	Asn	Gln 85	Leu	Gly	Ile	Ala	Pro 90	Gly	Asp	Leu	Ala	Ala 95	Ser		
Thr	Ser	Pro	Val 100	Asn	Ala	Gln	Gln	Gly 105	Ile	Ala	Asp	Gly	Asn 110	Asn	Trp		
Ala	Val	Gly 115	Gly	Tyr	Arg	Thr	Asp 120	Gln	Ile	Tyr	Asp	Ser 125	Ile	Thr	Ala	•	

Ala	Asn	Gly	Ser	Leu	Ile	Glu	Arg	Asp	Asn	Thr	Leu	Leu	Arg	Ser	Arg
	130					135					140				

- Asp Gly Tyr Leu Val Asp Arg Ala Arg Gln Gly Leu Gly Ala Asp Pro 145 150 155 160
- Asn Ala Leu Tyr Tyr Ile Thr Gly Gly Gly Asn Asp Phe Leu Gln Gly
 165 170 175
- Arg Ile Leu Asn Asp Val Gln Ala Gln Gln Ala Ala Gly Arg Leu Val
- Asp Ser Val Gln Ala Leu Gln Gln Ala Gly Ala Arg Tyr Ile Val Val 195 200 205
- Trp Leu Leu Pro Asp Leu Gly Leu Thr Pro Ala Thr Phe Gly Gly Pro 210 215 220
- Leu Gln Pro Phe Ala Ser Gln Leu Ser Gly Thr Phe Asn Ala Glu Leu 225 230 235
- Thr Ala Gln Leu Ser Gln Ala Gly Ala Asn Val Ile Pro Leu Asn Ile 245 250 255
- Pro Leu Leu Leu Lys Glu Gly Met Ala Asn Pro Ala Ser Phe Gly Leu 260 265 270
- Ala Ala Asp Gln Asn Leu Ile Gly Thr Cys Phe Ser Gly Asn Gly Cys 275 280 285
- Thr Met Asn Pro Thr Tyr Gly Ile Asn Gly Ser Thr Pro Asp Pro Ser 290 295 300
- Lys Leu Leu Phe Asn Asp Ser Val His Pro Thr Ile Thr Gly Gln Arg 305 310 315 320
- Leu Ile Ala Asp Tyr Thr Tyr Ser Leu Leu Ser Ala Pro Trp Glu Leu 325 330 335
- Thr Leu Leu Pro Glu Met Ala His Gly Thr Leu Arg Ala Tyr Gln Asp 340 345 350
- Glu Leu Arg Ser Gln Trp Gln Ala Asp Trp Glu Asn Trp Gln Asn Val 355 360 365

Gly	Gln	Trp	Arg	Gly	Phe	Val	Gly	Gly	Gly	Gly	Gln	Arg	Leu	Asp	Phe
	370					375					380				

- Asp Ser Gln Asp Ser Ala Ala Ser Gly Asp Gly Asn Gly Tyr Asn Leu 385 390 395 400
- Thr Leu Gly Gly Ser Tyr Arg Ile Asp Glu Ala Trp Arg Ala Gly Val 405 410 415
- Ala Ala Gly Phe Tyr Arg Gln Lys Leu Glu Ala Gly Ala Lys Asp Ser 420 430
- Asp Tyr Arg Met Asn Ser Tyr Met Ala Ser Ala Phe Val Gln Tyr Gln 435 440 445
- Glu Asn Arg Trp Trp Ala Asp Ala Ala Leu Thr Gly Gly Tyr Leu Asp 450 455 460
- Tyr Asp Asp Leu Lys Arg Lys Phe Ala Leu Gly Gly Glu Arg Ser 465 470 475 480
- Glu Lys Gly Asp Thr Asn Gly His Leu Trp Ala Phe Ser Ala Arg Leu 485 490 495
- Gly Tyr Asp Ile Ala Gln Gln Ala Asp Ser Pro Trp His Leu Ser Pro 500 505 510
- Phe Val Ser Ala Asp Tyr Ala Arg Val Glu Val Asp Gly Tyr Ser Glu 515 520 525
- Lys Gly Ala Ser Ala Thr Ala Leu Asp Tyr Asp Asp Gln Lys Arg Ser 530 540
- Ser Lys Arg Leu Gly Ala Gly Leu Gln Gly Lys Tyr Ala Phe Gly Ser 555 560
- Asp Thr Gln Leu Phe Ala Glu Tyr Ala His Glu Arg Glu Tyr Glu Asp 565 570 575
- Asp Thr Gln Asp Leu Thr Met Ser Leu Asn Ser Leu Pro Gly Asn Arg
 580 585 590
- Phe Thr Leu Glu Gly Tyr Thr Pro Gln Asp His Leu Asn Arg Val Ser 595 600 605

Leu Gly Phe Ser Gln Lys Leu Ala Pro Glu Leu Ser Leu Arg Gly Gly 610 615 620

Tyr Asn Trp Arg Lys Gly Glu Asp Asp Thr Gln Gln Ser Val Ser Leu 625 630 635 640

Ala Leu Ser Leu Asp Phe 645